

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:** Please **amend** the claims as follows:

**We claim:**

**Claims 1.–53. (Cancelled)**

**Claim 54. (Currently Amended)** A process for the production of ergosterol or an intermediate product thereof which is squalene, farnesol, geraniol, lanosterol, zymosterol, 4,4-dimethylzymosterol, 4-methylzymosterol, ergost-7-enol or ergosta-5,7-dienol or a sterol with a 5,7-diene structure, comprising fermenting into ergosterol with a plasmid vector-transformed yeast ~~microorganism~~, wherein said vector comprises suitable yeast genes of the ergosterol metabolic process in altered form, wherein the catalytic area of yeast HMG is expressed without its membrane-bonded domain; and the natural promoter of yeast t-HMG, yeast ERG9 and yeast SAT1 gene is replaced by the middle part of yeast ADH1 promoter, the suitable yeast genes being

a-i)

- i) a gene of the HMG-Co-A-reductase (t-HMG),
- ii) a gene of the squalene synthetase (ERG9),
- iii) a gene of the acyl-CoA: sterol-acyltransferase (SAT1), and
- iv) a gene of squalene epoxidase (ERG1),

or

a-ii)

- i) a gene of HMG-Co-A-reductase (t-HMG), and
- ii) a gene of the squalene synthetase (ERG9),

or

a-iii)

- i) a gene of the HMG-Co-A-reductase (t-HMG), and
- ii) a gene of the acyl-CoA: sterol-acyltransferase (SAT1),

or

a-iv)

- i) a gene of the HMG-Co-A-reductase (t-HMG), and
- ii) a gene of squalene epoxidase (ERG1),

or

a-v)

- i) a gene of squalene synthetase (ERG9), and
- ii) a gene of acyl-CoA: sterol-acyltransferase (SAT1)

or

a-vi)

- i) a gene of squalene synthetase (ERG9), and
- ii) a gene of squalene epoxidase (ERG1),

or

a-vii)

- i) a gene of acyl-coA: sterol-acyltransferase (SAT1) and
- ii) a gene of squalene epoxidase (ERG1),

or

a-viii) at least one of the genes of a-i),

and

analyzing, purifying and isolating the fermented product.

**Claim 55. (Currently Amended)** A process according to claim [[54]] 82, further comprising a gene of squalene epoxidase (*ERG1*) in a-ii), a-iii), and a-v), and a gene of acyl-CoA: sterol-acyltransferase in a-ii).

**Claim 56. (Currently Amended)** A process according to claim [[54]] 82, wherein the genes in a-i) to a-vii) are introduced, in each case independently of one another, into ~~microorganisms of the~~ same species of said yeast.

**Claim 57. (Cancelled)**

**Claim 58. (Cancelled)**

**Claim 59. (Cancelled)**

**Claim 60. (Cancelled)**

**Claim 61. (Currently Amended)** A process according to claim [[60]] 82, wherein said yeast is *S. cerevisiae*.

**Claim 62. (Previously Presented)** A process according to claim 61, wherein said yeast is *S. cerevisiae* AH22.

**Claim 63. (Currently Amended)** Yeast strain *S. cerevisiae* AH22, comprising one or more of the following yeast genes ~~genes mentioned under a i) of claim 54~~

~~a-i)~~

i) ~~a gene of the HMG-Co-A-reductase (t-HMG),~~

ii) ~~a gene of the squalene synthetase (ERG9),~~

iii) ~~a gene of the acyl-CoA; sterol-acyltransferase (SAT1), and~~

iv) ~~a gene of squalene epoxidase (ERG1).~~

**Claim 64. (Cancelled)**

**Claim 65. (Cancelled)**

**Claim 66. (Cancelled)**

**Claim 67. (Cancelled)**

**Claim 68. (Currently Amended)** An expression cassette that comprises the average yeast *ADH* promoter, the yeast *t-HMG* gene, the yeast *TRP* terminator and the yeast *SAT1* gene with the average yeast *ADH* promoter and the yeast *TRP* terminator.

**Claim 69. (Currently Amended)** An expression cassette comprising the average yeast *ADH* promoter, the yeast *t-HMG* gene, the yeast *TRP* terminator, the yeast *SAT1* gene with the average yeast *ADH* promoter, and the yeast *TRP* terminator, and the yeast *ERG9* gene with the average yeast *ADH* promoter and the yeast *TRP* terminator.

**Claim 70. (Currently Amended)** A combination of expression cassettes comprising

- a) a first expression cassette, ~~on which comprising the yeast *ADH* promoter, the yeast *t-HMG* gene and the yeast *TRP* terminator are located,~~
- b) a second expression cassette, ~~on which comprising the yeast *ADH* promoter, the yeast *SAT1* gene and the *TRP* terminator are located,~~

and

- c) a third expression cassette, ~~on which comprising the yeast *ADH* promoter, the yeast *ERG9* gene with and the *TRP* terminator are located.~~

**Claim 71. (Cancelled)**

**Claim 72. (Cancelled)**

**Claim 73. (Previously Presented)** A microorganism comprising an expression cassette according to claim 68.

**Claim 74. (Previously Presented)** A microorganism according to claim 73, which is yeast.

**Claim 75. (Cancelled)**

**Claim 76. (Cancelled)**

**Claim 77. (Currently Amended)** A process according to claim 55, wherein the genes are introduced, in each case independently of one another, into ~~microorganisms of the same species of~~ said yeast.

**Claim 78. (Previously Presented)** A microorganism comprising an expression cassette according to claim 69.

**Claim 79. (Previously Presented)** A microorganism comprising a combination according to claim 70.

**Claim 80. (Previously Presented)** A microorganism according to claim 78, which is yeast.

**Claim 81. (Previously Presented)** A microorganism according to claim 79, which is yeast.

**Claim 82. (Previously Presented)** A process for the production of ergosterol or an intermediate product thereof which is squalene, farnesol, geraniol, lanosterol, zymosterol, 4,4-dimethylzymosterol, 4-methylzymosterol, ergost-7-enol or ergosta-5,7-dienol or a sterol with a 5,7-diene structure, comprising fermenting into ergosterol with a plasmid vector-transformed yeast, wherein said vector comprises suitable genes of the ergosterol metabolic process in altered form, wherein the catalytic area of HMG-CoA reductase (HMG1) is expressed without its membrane-bonded domain; and the natural promoter of altered variant of HMG-1 (t-HMG), squalene synthetase (ERG9) and sterol-acyl transferase (SAT1) gene is replaced by the middle part of ADH1 promoter, the suitable genes being

a-i)

i) a gene of the HMG-Co-A-reductase (t-HMG),

- ii) a gene of the squalene synthetase (ERG9),
- iii) a gene of the acyl-CoA: sterol-acyltransferase (SAT1), and
- iv) a gene of squalene epoxidase (ERG1),

or

a-ii)

- i) a gene of HMG-Co-A-reductase (t-HMG), and
- ii) a gene of the squalene synthetase (ERG9),

or

a-iii)

- i) a gene of the HMG-Co-A-reductase (t-HMG), and
- ii) a gene of the acyl-CoA: sterol-acyltransferase (SAT1),

or

a-iv)

- i) a gene of the HMG-Co-A-reductase (t-HMG), and
- ii) a gene of squalene epoxidase (ERG1),

or

a-v)

- i) a gene of squalene synthetase (ERG9), and
- ii) a gene of acyl-CoA: sterol-acyltransferase (SAT1)

or

a-vi)

- i) a gene of squalene synthetase (ERG9), and
- ii) a gene of squalene epoxidase (ERG1),

or

a-vii)

- i) a gene of acyl-coA: sterol-acyltransferase (SAT1) and
- ii) a gene of squalene epoxidase (ERG1),

or

a-viii) at least one of the genes of a-i),

and

analyzing, purifying and isolating the fermented product.

**Claim 83. (Previously Presented)** The process according to claim 82, wherein said suitable genes of the ergosterol metabolic process are yeast genes.